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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/165,460	10/02/1998	JASPER D. RINE	B96-021-3	7914

23379 7590 02/21/2002

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EXAMINER
RAMIREZ, DELIA M

ART UNIT	PAPER NUMBER
1652	20

DATE MAILED: 02/21/2002

Please find below and/or attached an Office communication concerning this application or proceeding.

Advisory Action	Application No. 09/165,460	Applicant(s) RINE ET AL.	
	Examiner Delia M. Ramirez	Art Unit 1652	

--The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

THE REPLY FILED 24 January 2002 FAILS TO PLACE THIS APPLICATION IN CONDITION FOR ALLOWANCE. Therefore, further action by the applicant is required to avoid abandonment of this application. A proper reply to a final rejection under 37 CFR 1.113 may only be either: (1) a timely filed amendment which places the application in condition for allowance; (2) a timely filed Notice of Appeal (with appeal fee); or (3) a timely filed Request for Continued Examination (RCE) in compliance with 37 CFR 1.114.

PERIOD FOR REPLY [check either a) or b)]

a) ☑ The period for reply expires 3 months from the mailing date of the final rejection.

b) ☐ The period for reply expires on: (1) the mailing date of this Advisory Action, or (2) the date set forth in the final rejection, whichever is later. In no event, however, will the statutory period for reply expire later than SIX MONTHS from the mailing date of the final rejection.
ONLY CHECK THIS BOX WHEN THE FIRST REPLY WAS FILED WITHIN TWO MONTHS OF THE FINAL REJECTION. See MPEP 706.07(f).

Extensions of time may be obtained under 37 CFR 1.136(a). The date on which the petition under 37 CFR 1.136(a) and the appropriate extension fee have been filed is the date for purposes of determining the period of extension and the corresponding amount of the fee. The appropriate extension fee under 37 CFR 1.17(a) is calculated from: (1) the expiration date of the shortened statutory period for reply originally set in the final Office action; or (2) as set forth in (b) above, if checked. Any reply received by the Office later than three months after the mailing date of the final rejection, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

1. ☐ A Notice of Appeal was filed on _____. Appellant's Brief must be filed within the period set forth in 37 CFR 1.192(a), or any extension thereof (37 CFR 1.191(d)), to avoid dismissal of the appeal.

2. ☐ The proposed amendment(s) will not be entered because:

   (a) ☐ they raise new issues that would require further consideration and/or search (see NOTE below);

   (b) ☐ they raise the issue of new matter (see Note below);

   (c) ☐ they are not deemed to place the application in better form for appeal by materially reducing or simplifying the issues for appeal; and/or

   (d) ☐ they present additional claims without canceling a corresponding number of finally rejected claims.

   NOTE: _____.

3. ☐ Applicant's reply has overcome the following rejection(s): _____.

4. ☐ Newly proposed or amended claim(s) _____ would be allowable if submitted in a separate, timely filed amendment canceling the non-allowable claim(s).

5. ☐ The a)☐ affidavit, b)☐ exhibit, or c)☒ request for reconsideration has been considered but does NOT place the application in condition for allowance because: *see attachment*.

6. ☐ The affidavit or exhibit will NOT be considered because it is not directed SOLELY to issues which were newly raised by the Examiner in the final rejection.

7. ☒ For purposes of Appeal, the proposed amendment(s) a)☐ will not be entered or b)☒ will be entered and an explanation of how the new or amended claims would be rejected is provided below or appended.

   The status of the claim(s) is (or will be) as follows:

   Claim(s) allowed: *none*.

   Claim(s) objected to: _____.

   Claim(s) rejected: *31, 33-35, 37-39, 41-43, 45-46*.

   Claim(s) withdrawn from consideration: _____.

8. ☐ The proposed drawing correction filed on _____ is a)☐ approved or b)☐ disapproved by the Examiner.

9. ☐ Note the attached Information Disclosure Statement(s)(PTO-1449) Paper No(s). _____.

10. ☒ Other: *see attached references*

ADVISORY ACTION

1. Claims 31, 33-35, 37-39, 41-43, and 45-46 are pending in the application.

2. Applicants allege in the amendment filed in Paper No. 19, filed 1/24/2002, that the 103(a) rejection applied to claims 31, 33-34 and 41-42 over Rose et al. (GenBank accession number Z49617) in view of Nozaki et al. (US Patent No. 4,997,767) and the 103(a) rejection applied to claims 35, 37-38, 43, 45-46 over Lye et al. (GenBank accession number Z49260) are not in compliance with the notice requirement of 35 U.S.C. 132. According to the records of the instant application, two Notices of References Cited (PTO-892) have been sent to Applicant in Paper No. 11, mailed on 9/13/2000, and in Paper No. 16, mailed 3/27/2001, indicating that the cited references were sent to Applicant by the previous Examiner of record. Also, according to the records of the instant application, the reasons for applying said rejections have been extensively discussed in the previous Office Actions. In any event, copies of the Rose et al. and Lye et al. references (alignments) are being forwarded to Applicants with this action.

3. Applicants argue that the creation dates relied on by the Examiner to determine the public availability of Rose et al. (GenBank accession number Z49617, October 6, 1995) and Lye et al. (GenBank accession number Z49260, May 16, 1995) are not the dates when such references were available to the public. After communications with representatives of GenBank and EMBL, which is the database where these sequences were originally filed, it was indicated that the creation dates are the dates when these entries first become available to the public. According to their records, the creation dates for entries Z49617 and Z49260 are October 6, 1995 and May 16, 1995. Therefore, these references are considered valid prior art over Applicant's earliest priority date of August 7, 1996.

4. In regard to the 103(a) rejection of claims 31, 33-34, and 39, 41-42, which is discussed in previous Office Actions, Applicants argue that while the entire yeast genome had been largely sequenced at the time the invention was made and open reading frames were identified, the claimed compositions would be neither anticipated nor obvious. Applicants further argue that the instant invention requires the coding sequence to be operatively joined to a promoter and that there was no motivation to select an open reading frame of unknown function, link it to an operative promoter, and express it in a vector. These arguments have been fully considered but are not found persuasive because once an open reading frame is known, one of ordinary skill in the art is motivated to insert the open reading frame in a vector with an operably linked promoter in order to characterize the protein encoded by such open reading frame. The existence of many open reading frames of unknown function does not eliminate the motivation to insert the open reading frame sequence into a vector to characterize the protein. On the contrary, one of skill in the art is highly motivated to determine the function of proteins encoded by unknown open reading frames.

5. In regard to the 103(a) rejection of claims 35, 37-38 and 43, 45-46, which is discussed in previous Office Actions, Applicants argue that Lye discloses computer predictions of thousands of possible coding sequences and does not disclose any gene or gene product. Applicants also argue that the Examiner uses Applicant's own disclosure to select one of many Saccharomyces genes and to provide motivation to recombine it in an expression vector. Furthermore, Applicants argue that in the absence of any evidence for function, there would be no motivation to select out one of the thousands of yeast ORFs of unknown function. These arguments have been fully considered but are not found persuasive because once an open reading frame is known

or even predicted, one of ordinary skill in the art is motivated to insert the open reading frame in a vector with an operably linked promoter in order to characterize the protein encoded by such open reading frame. The existence of many open reading frames of unknown function does not eliminate the motivation to insert the open reading frame sequence into a vector to characterize the protein. On the contrary, one of skill in the art is highly motivated to determine the function of proteins encoded by unknown open reading frames. Constructing a vector comprising the polynucleotide of SEQ ID NO: 3 or a vector comprising a polynucleotide which will hybridize under stringent conditions to SEQ ID NO: 3, and transforming a host cell to express the corresponding protein would have been obvious to one of skill in the art at the time the invention was made once it was known that said sequence was an open reading frame. In response to Applicant's argument that the Examiner's conclusion of obviousness is based upon Applicant's disclosure, it must be recognized that any judgment on obviousness is in a sense necessarily a reconstruction based upon hindsight reasoning. But so long as it takes into account only knowledge which was within the level of ordinary skill at the time the invention was made, and does not include knowledge gleaned only from Applicant's disclosure, such reconstruction is proper. See *In re McLaughlin*, 443 F.2d 1392, 170 USPQ 209 (CCPA 1971). Moreover, the motivation disclosed in Applicant's disclosure is not the same motivation provided by the Examiner.

6. The request for consideration is acknowledged. The amendment filed on 1/24/2002 under 37 CFR 1.116 in reply to the final rejection has been considered but is not deemed to place the application in condition for allowance. For Appeal purposes, the status of the pending claims is as follows:

Claims allowed: NONE

Claims rejected: 31, 33-35, 37-39, 41-43, 45-46

Claims objected: NONE

7. Any inquiry concerning this communication or earlier communications from the examiner should be directed to Delia M. Ramirez whose telephone number is (703) 306-0288. The examiner can normally be reached on Monday-Friday from 8:30 AM to 5:00 PM.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Dr. Ponnathapura Achutamurthy can be reached on (703) 308-3804. Any inquiry of a general nature or relating to the status of this application or proceeding should be directed to the receptionist whose telephone number is (703) 308-0196.

Delia M. Ramirez, Ph.D.
Patent Examiner
Art Unit 1652

DR
February 15, 2002

PONNATHAPU ACHUTAMURTHY
SUPERVISORY PATENT EXAMINER
TECHNOLOGY CENTER 1600

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: February 12, 2002, 13:20:11 ; Search time 4622.84 Seconds
(without alignments)
10520.305 Million cell updates/sec

Title: US-09-165-460A-3
Perfect score: 2948
Sequence: 1 tgaactgttgatgaacaaag.....ggggaggataaagaatcaca 2948

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_om:*
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24: em_pl:*
25: em_ro:*
26: em_sts:*
27: em_sy:*
28: em_un:*
29: em_vi:*
30: em_htgo_hum:*
31: em_htgo_inv:*
32: em_htgo_rod:*
33: em_htg_hum:*
34: em_htg_inv:*
35: em_htg_rod:*
36: em_htg_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	Query Match	Length	DB	ID	Description
c	1	2948	100.0	29987	8	SC8156	Z49260 S.cerevisia
	2	1560.4	52.9	4156	8	D50276	D50276 Saccharomyc
	3	1361	46.2	4130	8	YSCNCR1G	L42821 Saccharomyc
	4	1163	39.5	4225	8	SCU65682	U65682 Saccharomyc
	5	1069.4	36.3	3250	8	SCU32580	U32580 Saccharomyc
	6	931	31.6	3525	8	SCU63849	U63849 Saccharomyc
	7	786.8	26.7	3240	8	YSCBUL1	D50083 Yeast BUL1
	8	703.8	23.9	3020	8	SCRDS1GEN	X88901 S.cerevisia
	9	225.2	7.6	270	8	YSCGENC58X	M87379 Yeast Eco
	10	143.8	4.9	27559	8	SC8339	Z49210 S.cerevisia
c	11	75	2.5	2023	8	SCYNR068C	Z71683 S.cerevisia
	12	71.8	2.4	4775	8	SCU32938	U32938 Saccharomyc
c	13	68	2.3	780	11	CNS06K8B	AL402561 T7 end c
	14	65.6	2.2	256172	2	AC005139	AC005139 Plasmodiu
	15	65.6	2.2	310779	2	AC005140	AC005140 Plasmodiu
	16	64.4	2.2	904	11	CNS06I89	AL399967 T3 end c
	17	64.4	2.2	86827	3	PFMAL3P5	AL034556 Plasmodiu
	18	63.4	2.2	1920	3	PFGTUB	X62393 P.fa aru
	19	63.4	2.2	110000	2	PFMAL13P2_0	AL049185 Pl diu
	20	62	2.1	253305	3	PFMAL3P7	AL034559 Plasmodiu
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	22	60.8	2.1	234112	3	PFMAL4P2	AL035475 Plasmodiu
	23	60.6	2.1	202872	2	AC016160	AC016160 Homo sap
c	24	60	2.0	5632	3	AF310892	AF310892 Dictyoste
c	25	59.4	2.0	3214	3	AF019980	AF019980 Dictyoste
	26	59.4	2.0	318221	2	PFMAL13P3	AL049184 Plasmodiu
	27	58.8	2.0	321003	2	PFMAL4P3	AL035476 Plasmodiu
	28	58.4	2.0	78439	17	HSU85197	U85197 Homo sapie
c	29	58.4	2.0	169546	2	AC004157	AC004157 Plasmodiu
	30	58.4	2.0	245802	2	AC006279	AC006279 Plasmodiu
	31	58.4	2.0	251124	9	HUAE000660	AE000660 Homo sapi
c	32	58.2	2.0	153098	3	PFMAL3P2	AL034558 Plasmodiu
	33	58	2.0	169794	2	AC004688	AC004688 Plasmodiu
	34	58	2.0	178137	9	AC011302	AC011302 Homo sapi
c	35	57.8	2.0	13684	3	AE001403	AE001403 Plasmodiu
	36	57.8	2.0	153477	2	AC006278	AC006278 Plasmodiu
	37	57.6	2.0	53932	2	AC023371	AC023371 Homo sapi
c	38	57	1.9	12029	3	AE001431	AE001431 Plasmodiu
	39	57	1.9	163443	2	AC006280	AC006280 Plasmodiu
c	40	57	1.9	178273	2	AC005308	AC005308 Plasmodiu
c	41	57	1.9	196149	2	AC004709	AC004709 Plasmodiu
c	42	56.8	1.9	67970	3	PFMAL1P3	AL031746 Plasmodiu
	43	56.8	1.9	149627	9	AC087428	AC087428 Homo sapi
c	44	56.6	1.9	92633	2	PFMAL4P1_3	Continuation (4 of
c	45	56.6	1.9	153477	2	AC006278	AC006278 Plasmodiu

ALIGNMENTS

RESULT 1
SC8156/c
LOCUS SC8156 29987 bp DNA PLN 11-AUG-1997
DEFINITION S.cerevisiae chromosome XIII cosmid 8156.
ACCESSION Z49260 Z71257
VERSION Z49260.1 GI:809081
KEYWORDS BUL1; cytochrome b5; DAG1; initiation factor 1A; inorganic pyrophosphatase; IPP2; nitrate reductase; orotate phosphoribosyltransferase; tau element; TIF11; TPS3; transfer RNA-Gln; trehalose-phosphate synthase; U6 snRNP; URA10.
SOURCE baker's yeast.
ORGANISM Saccharomyces cerevisiae
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
REFERENCE 1 (bases 1 to 29987)
AUTHORS Lye,G. and Churcher,C.M.
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 29987)
AUTHORS Barrell,B. and Rajandream,M.A.
TITLE Direct Submission

JOURNAL Submitted (12-MAY-1995) Saccharomyces cerevisiae chromosome XIII sequencing project, Sanger Centre, Hinxton Hall, Hinxton, Cambridge CB10 1RQ E-mail: barrell@sanger.ac.uk

COMMENT Notes:
All CDS over 100 codons have been analysed. CDS that are completely overlapped and those that are overlapped by more than 50% of their length by a larger CDS have been omitted from this analysis.
Details of the omitted CDS are available on request. The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length in codons and the calculated codon adaptation index (CAI) is given for each CDS.
Cosmid 8156 is overlapped at the start by cosmid 9920, embl entry SC9920, accession no. Z48639 and at the end by cosmid 8021.

FEATURES Location/Qualifiers

source 1. .29987
/organism="Saccharomyces cerevisiae"
/strain="AB972"
/db_xref="taxon:4932"
/chromosome="XIII"
/clone="cosmid 8156"
/map="13R"

CDS complement(<1. .356)
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/translation="MTTDVQFSSQEIELFRVKEFLIANNPAKINNENKDAVLTQIEHD
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CDS complement(851. .1312)
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gene complement(1678. .4842)
/gene="TPS3"

CDS complement(1678. .4842)
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NNKQERSSSVTSASSHYIGLPQEAQINGEPLQRANVGSPATGVNYHNEMEMLSSEQFL
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SRSSAHHNDLSSSLMKNPNLSFDSHPPRVRSSSKSAVITPVSKSVPDVDPAVVDVAKV
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/product="unknown"
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PEPLDLEEYIKREFNDTLVSVIGEIGLDKLFRLPANGFYMQNEKARLTTVKVKLSH
TVFRRFWRLARHTSKPISIHDVRCHGKLNDICNEELLTYHSVKICLHSYTGSKETLF
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CDS 6392. .6997
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CDS 7278. .7889
/note="YM8156.06, unknown, len: 301, CAI: 0.13, SW:YTP1_YEAST P38428, extends previously noted ORF"
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CDS complement(8013. .9398)
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RFNAVCLKKRAISEYTSKYKKELMRDFLEYYPSLRELSIYDDRIHQIDAFKSFFHSLD
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CDS 9991. .12852
/note="YM8156.08, unknown, len: 953, CAI: 0.20, probable integral membrane glycoprotein"
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Query Match 100.0%; Score 2948; DB 8; Length 29987;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2948; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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D50276
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DEFINITION  Saccharomyces cerevisiae HST1 gene, complete cds.
ACCESSION   D50276
VERSION     D50276.1  GI:1777313
KEYWORDS    HST1; high-copy suppressor of TFP sensitivity.
SOURCE      Saccharomyces cerevisiae (strain:RAY-3A) DNA.
  ORGANISM  Saccharomyces cerevisiae
            Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
            Saccharomycetales; Saccharomycetaceae; Saccharomyces.
REFERENCE   1  (bases 1 to 4156)
  AUTHORS   Tsuchiya,E.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-APR-1995) to the DDBJ/EMBL/GenBank databases. Eiko
            Tsuchiya, Hiroshima University Faculty of Engineering, Department
            of Fermentation Technology; Kagami-yama, Higashi-Hiroshima,
            Hiroshima 739, Japan (E-mail:etsuchi@ipc.hiroshima-u.ac.jp,
            Tel:0824-24-7868, Fax:0824-24-7868)
REFERENCE   2  (bases 1 to 4156)
  AUTHORS   Tsuchiya,E., Matsuzaki,G., Tsukao,A. and Miyakawa,T.
  TITLE     Molecular cloning and characterization of S. cerevisiae HST1 gene
  JOURNAL   Unpublished (1995)
REFERENCE   3  (sites)
  AUTHORS   Tsuchiya,E., Matsuzaki,G., Kurano,K., Fukuchi,T., Tsukao,A. and
            Miyakawa,T.
  TITLE     The Saccharomyces cerevisiae SSD1 gene is involved in the tole ice
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  JOURNAL   Gene 176 (1-2), 35-38 (1996)
  MEDLINE   97075905
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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: February 12, 2002, 10:38:12 ; Search time 4622.84 Seconds
(without alignments)
6512.739 Million cell updates/sec

Title: US-09-165-460A-1
Perfect score: 1825
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_htg:*
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36: em_htg_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	342	18.7	1555	8	SCYJR116W	Z49616 S.cerevisia
c 4	195	10.7	99360	8	NCB11N2	AL513444 Neurospor
5	187	10.2	36920	8	SPAC3H1	Z68144 S. pombe ch
6	137.2	7.5	1275	8	AF353722	AF353722 Arabidops
c 7	136	7.5	686	6	A86270	A86270 Sequence 92
c 8	136	7.5	686	6	AR155763	AR155763 Sequence
c 9	136	7.5	686	6	E66288	E66288 Genome DNA
10	121	6.6	935	8	SCYJR118C	Z49618 S.cerevisia
11	117.4	6.4	1859	9	AF064867	AF064867 Homo sapi
12	117.4	6.4	2963	9	AB016068	AB016068 Homo sapi
13	117.4	6.4	2966	9	HSY13834	Y13834 Homo sapien
14	117.4	6.4	2968	6	E32056	E32056 Human AFC1.
15	114.2	6.3	1340	3	AF358443	AF358443 Physarum
16	98.4	5.4	78592	3	AC004335	AC004335 Drosophil
17	98.4	5.4	102413	2	AC020024	AC020024 Droso[illegible]1
c 18	92.8	5.1	41327	3	CBRG47J19	AC084676 Caen[illegible]
c 19	91.6	5.0	40767	3	CEC04F12	Z81461 Caenori[illegible]i
c 20	88	4.8	317511	1	CJ11168X3	AL139076 Campyloba
21	86.6	4.7	582	8	CNS018PP	AL110644 Botrytis
22	81.6	4.5	660	8	CNS01AH3	AL112927 Botrytis
23	72.2	4.0	2161	9	AK027874	AK027874 Homo sapi
24	66.8	3.7	1072	6	AX055334	AX055334 Sequence
c 25	66.6	3.6	124808	2	AP000652	AP000652 Homo sapi
c 26	65.6	3.6	16488	1	AE004992	AE004992 Halobacte
27	65	3.6	256172	2	AC005139	AC005139 Plasmodiu
c 28	64.4	3.5	169423	2	AC069309	AC069309 Mus muscu
c 29	64.4	3.5	186306	2	AC083946	AC083946 Mus muscu
30	63.6	3.5	1245	6	AX055202	AX055202 Sequence
c 31	63.6	3.5	19715	1	AE000555	AE000555 Helicobac
c 32	63.6	3.5	234112	3	PFMAL4P2	AL035475 Plasmodiu
33	62.4	3.4	13383	3	AE001374	AE001374 Plasmodiu
c 34	61.8	3.4	98734	2	PFMAL1P2	AL031745 Plasmodiu
35	61.6	3.4	14943	1	AE001528	AE001528 Helicobac
36	59.8	3.3	12029	3	AE001392	AE001392 Plasmodiu
37	59.8	3.3	110000	2	AC087899_0	AC087899 Mus muscu
c 38	59.2	3.2	114736	3	PFMAL3P3	Z98547 Plasmodium
39	59.2	3.2	253305	3	PFMAL3P7	AL034559 Plasmodiu
40	58.8	3.2	98899	2	AL603743	AL603743 Danio rer
41	58.8	3.2	318221	2	PFMAL13P3	AL049184 Plasmodiu
c 42	58.8	3.2	318503	2	AC074166	AC074166 Mus muscu
c 43	58.4	3.2	172239	2	AC069587	AC069587 Homo sapi
44	58.2	3.2	12029	3	AE001412	AE001412 Plasmodiu
c 45	58.2	3.2	187469	9	AL357312	AL357312 Human DNA

ALIGNMENTS

RESULT 1
SCYJR117W
LOCUS SCYJR117W 1825 bp DNA PLN 11-AUG-1997
DEFINITION S.cerevisiae chromosome X reading frame ORF YJR117w.
ACCESSION Z49617 Y13136
VERSION Z49617.1 GI:1015836
KEYWORDS .
SOURCE baker's yeast.
ORGANISM Saccharomyces cerevisiae
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
REFERENCE 1 (bases 1 to 1825)
AUTHORS Rose,M., Koetter,P. and Entian,K.D.
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1825)
AUTHORS MIPS.
TITLE Direct Submission
JOURNAL Submitted (25-SEP-1995) Data collected by MIPS on behalf of the
European yeast chromosome X sequencing project. MIPS at the
Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a D-82152

Martinsried, FRG; E-mail: Mewes@mips.embnet.org

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FEATURES             Location/Qualifiers
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                     PMFNKFTPLEDGELKKSIESLADRVGFPLDKIFVIDGSKRSSHSNAYFTGLPFTSKRI
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BASE COUNT       570 a    397 c    280 g    578 t
ORIGIN
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Query Match 99.9%; Score 1823.4; DB 8; Length 1825;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1824; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      61 acatacatacatacaaatatacatatatgtaaacttgtatattcattcctattaaccaaa 120
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Qy     181 tcgtctctgttctgccatttttctccagaaaaaaatcgacgggaaataaaaaaaaaaagac 240
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Qy     241 aacgaacaagagaaaaagttcgcgaattataaaccacttctataattaacaggaaaagga 300
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Qy     361 attctcgaccatcctaatatcccgtggaaattaatcatttctgggttctcgattgcccaa 420
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Qy     421 ttttctttcgaatcttacttgacgtacagacagtaccagaagctatctgaaacaaagttg 480
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Qy     661 gtcctgccagtcagatttcatatggtctccactgtcgcacagagtttatgcttcttgggt 720
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Qy    1261 atcgttaatatggtcatctttagtcaattgcacaccttcctcattttctccccttttcacc 1320
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RESULT   2
SCU77137
LOCUS       SCU77137     1706 bp    DNA             PLN       07-DEC-1996
DEFINITION  Saccharomyces cerevisiae zinc metallo-protease (STE24) gene,
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ACCESSION   U77137
VERSION     U77137.1  GI:1679740
KEYWORDS
SOURCE      baker's yeast.
  ORGANISM  Saccharomyces cerevisiae
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            Saccharomycetales; Saccharomycetaceae; Saccharomyces.
REFERENCE   1  (bases 1 to 1706)
  AUTHORS   Fujimura-Kamada,K., Nouvet,F.J. and Michaelis,S.
  TITLE     A novel membrane-associated metalloprotease, Ste24p, is required
            for the first step of N-terminal processing of the yeast a-factor
            precursor
  JOURNAL   J. Cell Biol. (1996) In press
REFERENCE   2  (bases 1 to 1706)
  AUTHORS   Michaelis,S. and Fujimura-Kamada,K.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-NOV-1996) Cell Biology and Anatomy, Johns Hopkins
            University School of Medicine, 725 North Wolfe Street, Baltimore,
            MD 21205, USA
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BASE COUNT      494 a    366 c    275 g    571 t
ORIGIN


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Qy    331 aggcctttattcatgtttgatcttaagacgattctcgaccatcctaatatcccgtggaaa 390
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Qy    931 tacattatggtcttcttgttcgttgtccaaatcttagccatgacaatcattccagtcttc 990
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Qy    991 atcatgcccatgtttaataagttcactccattggaggacggtgaactgaaaaaatctatt 1050
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Qy   1111 aaaagatcttctcattcaaacgcatatttcacaggtttgccattcacctccaagagaatt 1170
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Qy    1801 aagaaaaaataaacgattaaacatt 1825
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RESULT   2
SCU77137
LOCUS       SCU77137     1706 bp    DNA             PLN       07-DEC-1996
DEFINITION  Saccharomyces cerevisiae zinc metallo-protease (STE24) gene,
            complete cds.
ACCESSION   U77137
VERSION     U77137.1  GI:1679740
KEYWORDS
SOURCE      baker's yeast.
  ORGANISM  Saccharomyces cerevisiae
            Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
            Saccharomycetales; Saccharomycetaceae; Saccharomyces.
REFERENCE   1  (bases 1 to 1706)
  AUTHORS   Fujimura-Kamada,K., Nouvet,F.J. and Michaelis,S.
  TITLE     A novel membrane-associated metalloprotease, Ste24p, is required
            for the first step of N-terminal processing of the yeast a-factor
            precursor
  JOURNAL   J. Cell Biol. (1996) In press
REFERENCE   2  (bases 1 to 1706)
  AUTHORS   Michaelis,S. and Fujimura-Kamada,K.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-NOV-1996) Cell Biology and Anatomy, Johns Hopkins
            University School of Medicine, 725 North Wolfe Street, Baltimore,
            MD 21205, USA
FEATURES             Location/Qualifiers
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ORIGIN


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